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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lavi, Sara
- (ii) TITLE OF INVENTION: MANIPULATION AND DETECTION OF PROTEIN PHOSPHATASE 2C -PP2CALPHA- EXPRESSION IN TUMOR CELLS FOR CANCER THERAPY, PREVENTION AND DETECTION
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Kohn & Associates
 - (B) STREET: 30500 Northwestern Hwy.
 - (C) CITY: Farmington Hills
 - (D) STATE: Michigan
 - (E) COUNTRY: US
 - (F) ZIP: 48334
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kohn, Kenneth I.
 - (B) REGISTRATION NUMBER: 30,955
 - (C) REFERENCE/DOCKET NUMBER: 2290.00037
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn	Asp	Asp	Thr	Asp	Ser	Ala	Ser	Thr	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asn Lys Asp Asn Asp Gly Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGATCAAGT CATAATGGGA

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(iv) ANTI-SENSE: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTGGAGTCT GATTTACAAC

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAAGTAGTCG ACACCTGT

18

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTTGAGACC TTCAACACCC C

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGGCCATCT CTTGCTCGAA GTC

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ala Phe Leu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGATCCGC ATGGGAGCAT TTTTAGAC

28

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Asp Asp Met Trp
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGGATCCT TACCACATAT CATCACT

27

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Silencer Region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTCCATCAC TAGGGGTTCC TGGAGGGGTG GAGTCGTGAC GTGAATTACG TCATAGGGTT	60
AGGG	64

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Mini-silencer region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTCCCATCA CTAGGGTTC CT	22
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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "35-3.seg (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTTGTCA AAATTACTAT TCAGTGTGAT TTTTAGTGGA TGAAACCTCA TGACTAGTAT	60
ATTATGACAT TAGCTTGCG TAGTGAAGGC ACAAGCTGCT AAGTGGTTAG GGATGTATT	120
TGCCGTAGCC TGTATCACNC CAGGTCTGG GCTCGTTCC TAGCATTACA GGAAAAAGCA	180
GGCGGTGGTT GACCTTTAAT GAATGGATT TTCAATTAG AAGTTGGTTT CATTTAAAG	240
AATTCAAAAA TGTCCCCAT AGCACTTTGT TTTGACATTG AGATCAGCTG CTAATTGAGG	300
TCCAGTATAT ACTTAGAAAA CTGAGCGAAA CTTTGATGGA CACACACACA CACCCCTGTT	360
GTTCATTAA TAATTGAAC TAAATAAAATA CTGTTAGTC ATCCACGTAA GCAAGAGGCC	420

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TGTGTAAACA GTATTTGTAT TAGTAAAAAC TTTATAACAT AGTTACATAA TCAGCATCAT	480
TTTTTTATG GACCTTATAG TTGGCTACTT CACTGGGTTT GTTATAATTT AATCAGACTC	540
CTAAATAGGT TAAATTTCTG AATTGCCTAC TTCAGTTTG AAGAATTATT TTGTTTCATA	600
ATTTCCCATG CATATCTGGT AAATAATTCT GGATTGTTTC TAAAGGGGAG AGCAAGGTCT	660
CTTATGAAA GTGAAAATCT AGATATGCTG TTTGTAAGAA TATAATAGTG ATAAAGTAGT	720
GTCCTTTIGC TCAGTGCCTC CATTCTTACC AGGCTGTGAC TGATCTTCAG TATTATTCA	780
ACAGTCACTA TTAATATATC CGTTGCACAG TGGGAAATT GAGGGAAGTT AGATAGGCAT	840
CGGGTATCTT AATCATAACT CACATATAACC CAGCTGGCTA GTCAAGCCTAG CTAAGACAGT	900
TCACACCCAG TTGAGGCAGC TTGCTGTTGG CCATTAGTAG GTAACCTTAAT GGCTTGGTTT	960
CTTCACTGGT AAGGTGGGGA TATAATAATG CCAATAATTG CATAATGATT AAAGACATTA	1020
ATATATTCCA TAAAATTCC TGAATAGTGC TTAGCTGGTA CCCCTCCCCA CACATGCACC	1080
CCAGTCCAAT GTTCAGATGT TTACTTTGTT AAGCCCAGTT AATCCATTCC CCCTAATATC	1140
TTCTCCCAGT TTGAAGAANG TTGAAGAATG TTGGGCTTGT TAGTTTAATT TTTTAAGAAG	1200
CATATCATGT TGCTTTTTA AAACATGTTT CTTTGGGTTT TGGCTTCCCC TTTTGGAAAG	1260
AATTCCAATT TACACTTATG GAAGAAAGCC ATTGTCCCCCT CCAATTCCC CCCCTGTCCC	1320
TTTCCAATAC AGCCCAAATC CCCATGTTT GACTTCCTCC CCTGAACCAC CCCGTTCTCC	1380
TGTTTTICCC TCCCCCANAA AAAAACCCCA ATAATTGAC TTTGTAATT GAATTTCGG	1440
CCNGTTAGGC NCCTGAATTG CCGAAATAAT TCCCCCGTGC NCCCNNGGANT TTTGGCACCC	1500
CCTGCCCTT AACCTGTTCT GCTGCCCTTCC ATTTTTAAAT GGCTTGCCTGC NTTACNCAA	1560
ANACTGCCTT TCC	1573

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "35-T7.seq (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCGATCTCA CAAAGTCACA GAGCTCTTCG TTTCCCATGA CATCCAGAT ACCATCACAT	60
GCAAGAATAA TGAACGTGATC GTCTCTTCA GACCTTCAA TATCATGGAC TTCTGGCTCT	120
GGTGAGACGA GCTGCTCTGT GGGACCTTTT CCATGGACAC ATTTGTAATC GAAATCCCCA	180
AGGGCCCTTG ACACAGCCAG AGAGCCATT ACACGCTGAA TCATCACAGA GCCCCCTGCA	240
TTCTGAATTC GTTCTTTTC CAGCGGGTTA CTTGGTTGT GGTCTTGTGT GAAGAAGTGA	300

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ACTTTCCGT TTCTACAAAG CAAACCTCTC GAGTCTCCAC AGTTAATGAA GTAAGTATGT	360
TTGGGGAGAA ATTAAGACCC CCACAGCTGT TTGACCCACT TCCTATCTGC ACCATGTTTT	420
CCTTCCTCCT GACATGACTC CTCATGTTGT TTCCATCAAT CTCCCAGAAA AACCTGTTCC	480
TGATCCCCAT TCCTTACAT TTTCCCACAG AAAGGTGCTC CCTGCAGAGC CTTTTAAAAT	540
CCCTGGTTTA TTGGTGATGT TGATTCTNAA CAAATGCTCC ACAGCCAGTA TTTNGGCAAC	600
CTTGAAAAAC CAGCATGCCC ATCCATATAC AGCCAAGAAT GACCAGTTC TCCAGTTCCA	660
CTTNTGGCAA ACCCAATCCA CAGCCGTNT GCGCATCCTC CCATTTCAAC TCCGCCAAC	720
CNTTGCNTGC TGCNTTAAGC CATATCGCAA CCCATCCCC CTGCCCTG GGGCATTATG	780
CNTTTCCATC TTTGGTTGTC TAAAATGCTC CCATTATGAC TTGATCCTCT AGGTCTGCAA	840
AGGAAGAGAA ATAAGAAAGT TAGTAACTGT CTTTGAAACA AAGCACACAT CCAACAGTCT	900
TTTGAAAGCA CCTACGAGAT ACAAGGAAAC GTAAAAACTC ATAGGCTATA GCCATAAGCA	960
TTGTTCTACT GACTTGGAAA ATGTAGAGAT TAATAAGAAA GGGAAAGGCT GATCAAGTAC	1020
AGCTCAACCA GACAAGCAGC AGATGGAAC AAGTCACCAAG GTAAAAGAGA GCTTGTGTC	1080
CTCTCTGTGA TACCAAGGAG GCCCAGCAGT GACCATTAAAC TTACATGAAC TAGGCAAGAT	1140
TTCAGGGTGC ATTCACTATA TGTAACCTCT CAATTAAGTT GTGTGTTGAT TAAAAAAAAT	1200
AATTCACTAGA AACATACAAG TATCTACTAC TTCAGGGAAC CTTAGCTAAG TACTCAGGAA	1260
TGTTGAGAGT TTGATTCCAT GCTATTTAGT TTTGTTCTA CAACTAGATA CCTTTGGTAA	1320
AAATAAAAAG TAATTACTCA CACTGGTCCA AATTTTCAGT GCCTTGTGCA GGTCATTCTC	1380
TTTAGCTGGA ATTCCCTGCC TCACCTCTT ACCAACAGAA AAAAATACA CCTGTTCTA	1440
TCCTTGAAA TCCAGTTCAA TTGTTCCCCC TTCTCCAGA CTTTACAGTC CTTGAAAAAA	1500
ACAAGTTATT AACTACAGAA GTCAGCTTCC ATTTCCAGTT NGGAATGTTT TTTAATGAAC	1560
AATTTTATTG TTCNAAAATCT NACNATATGA TAACTAANCN AATGGTAATA ATATTTCAN	1620
CCCTGCCCTA TGGCCGCTNT TTTTAATCCT NAAAAAAATC NAAGGTCTAT TCCNCCNNC	1680
CTTGCCAATA CTTNACANCN CCAGTTCCCT GATCTGGAAT GGACCCACAA AGGTCAAGAC	1740
TTAGGTTANC CTTGCTCAC AAACTAAAGA AAATCTAAA GGAGAACAGA ATACTGAAGA	1800
GAGAAATGAG GGTGAAGGAC AGTGTTCAGG TGACGTTCTG AAACCAGGG ACTAAANATA	1860
CCANAANTGG TGTTNCAGAC AGAAATGGTA TGGAAAACTC CTTAGGAAAG AAATGACANN	1920
TNTTGTGTCG CAGCAACCCC CNACATGGC TTTCTCTTT TCCTTCTGCT GATTAACTGA	1980
TGCACNTGGT ANAAAAGTCA ACANACCCCT CCTCCACNCA GACTCCCACC GAGTACANNG	2040
GCCCATGTGC TCANTACACT CTGCCCTAAA CTCNNANNAT TCATTCNNCT CCCCNTGTNA	2100
TTTATNAGGG CCTTTCCCN CAGTTNTCTN ATCNCCAACG GANATTANCC TTCCANNNNAT	2160
TTACCCCCNN TTTGTACANC ACATNNNTGGC NNGTGCCACN GTTANGCGTC GGCNTCCCTG	2220
TTNCACTNCA TCCCTCATCN TTAGGCCANG TTTGATTCTC CNGTGCANAN TTTCCGCANN	2280

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ANCNTACCCC TTGCACCN	TCATNTCTNNG GAANAAACCTC CGGTTCTGAA TCTNCC	2340	
CCCCGT	CNCT CCCCN	TTCTTTCTC TANTTTTTC CNNGGNACGG GTTGNGGTNA	2400
ATNAANN	CCCCTCGTC TATT	CANCCC TTCCTATGNA CACTTCCTGN CCCCTATCT	2460
CTCTATNTNC	TNCTCTCAT ATCTNNATCC	CNTCTTCNCN TGCCNCTCCC TNGTN	2520
NCGGGTATT	TTTNTTCTCC TCNTCTTCTT	CCCCTNTNTA NCCNTNCTNC NNNC	2580

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 830 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "5H-1 (Example 10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGGGAGAG GACTGAAATA	TTTCCACAGC CTTTTTATTG GTGGTGATGG TAGTGATGGT	60
TAGGATTCC	TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC TTTCTTTTTT TTTTTTTTTT	120
TTTTTTTTT	GAGACAGGGT TTCTCTGGGT ACTCCTGGAA CTCACTTTGT GGACCATGAA	180
TGACATGAAT	ACTTCGATAT ATACATACAT ACAAAAGACAC ATATTTTAA AAAGAGAATT	240
AGAGTAGAGC	TGGGGCAATT GTGGAACACA CCTTTAACCT CAGGCAGATT TCTGCGTTCA	300
AGGTCACCTT	GGATTACAAG GCAGCTAGGG CTACACAGAG AAACCATATC TCAAAAAAAA	360
GAAAAAATAA	TGAAAGAAAG AAAGGAAGGA AGGAAGGAAG GAAGGAAGGA AGGAAGGAAG	420
AAAGGAAGGT	AGGAAGAAAG GTATTTCTT AAAAAAAAAA AAAAAAAAAA TTTATTCCGG	480
GCAGTGGTGG	CAAATGCTTT TAATCCCACC ATTTGGAAA GCAGAGGCAG ACAGATTAAA	540
TTTCAAGGC	CCACCTGGTC CTACACAGTG AATTCCAGGA ACACCTAGGT TTACCCANAA	600
AAAACCCCCC	CTTGAAATAA ACAAAAATAA ATTAAATAAA TAAAATTAA AAATAAAACC	660
CGGGCGTTAA	ACCCNCTTTT ATCCCCCAC TTNGGAAGCA AAAGCCGGCN GATTCTGAA	720
TTCNAGGCCN	CCCTGTCTAT GAATTANTTC CCNGAACACC CNAATTTC NAAAAACCCC	780
CCNTTTCTTA	AAAAANCCAA ATTATTATTN ATTAATTAAA TNAAATTACC	830

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "AN8T7 (Example 10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGTCCAAC AATGGTTCC ACTTGTCTGG CGGCCGCTCT AGAGTTCCC ATAAGCTGGA	60
CTGAGAGATG GTGTGATTGC TGTGGGTGAC AAAGACAGAG GCACCTTCATA TCTCTACCC	120
TCTCTTGTGTT TGTTGTTTGT TTGAGACCGG TTCCCACATAT GTAGACCAGG CTGGAGGACA	180
GGGTCTCACT ATGTAGACCA GGCTGGCCTT GAACTCAAAG ACATCTGCCT GCCTCTGCCT	240
CCTGAGGGCT GGGATTAAAG GCGTGTGCTG CCACTGACAG CTTCTATCCT CCTGTCATCA	300
GTCCCCGGCTC ACAGGGCCAG AAGATCTCTT CTATGCTTCC ACTATTTCCC CAATCCATTC	360
CCACGGCAGC CTCTCCATCT CCCTACCACC AAGACAGCAG CCTAGTGATA TAACAAAACT	420
TTTATTCAACA GGAAACCGGA AAACAAAATC ACAACCAATC ATTTCTATCT AGTCCCTGCC	480
CTAGCCCTCC CTCCAAGCCC CTACATATCC TCCATCTGAG GGGGATGCAT GCGTTGGGTG	540
GGAGCTGCCG GCATCCTTAT CCTGGTTCCCT GGAGTAGNGA AGAGTGGTTC TTTTCAACGN	600
CTAGGGNNCT CCCCTCCAAG TTNGGACCTC TCTTCCCAGG NCTTCNCCCC TCCCTNACAG	660
GGNACAAAAAA ACCAGGNACG GCACNACGCC AGGNAGGAAG GGACTCTTGG NAATGTTGGG	720
CAGGACTTGT CCTCAGAATT CCNNGGAGGA ATCAAGGGCC TTGAATTGG GAACCACTNC	780
CGAGGNCTTC ANCANGGCAN AGTCATTT TCCATCCCGG TTGGCCANC CTGGCCNG	838

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "CHINT (TABLE 5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGTGCCGGT CAAGGAACGT AACGTGCGAT TCCGGGACAG GCTACCCACT CCGATCCCAG	60
GAGAAGTTGT CATGGTGAGG GCCACCCCTAG GTCTCTGCCCT CTGCTGTGTC CCCCATCTTA	120
CCCACATCCAGT AGGATCTAGA GGCTGTCGCC CCCTTGTGGA ATGCCACAGAA GTCACAAAGCG	180

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "HUMMDB (TABLE 5)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCACCTCC	GCCCTGTTTC	GTCCAGGTCC	TCCGGGTCA	GCTACCCCCG	TCGCCGCCAG	60
AGCGCGGGGG	AGGGGAGAGC	TTCTTTGTC	TCCTATGCCT	CCTCCCCCA	TCCC GGCTCT	120
CCTGC GGGCA	AGCGCCGAGG	GGACACCGGG	GAGTACCCCA	CCTGAACCTC	TGGGG	175